Amendments to the Claims

This listing of claims will replace all prior versions and listings of claims in the application:

Claims 1-3 (cancelled)

4. (Currently amended) A method for generating a secondary library of scaffold protein variants comprising:

a) generating a library of primary sequences utilizing an alignment program;

b) generating a probability distribution ~~table of~~ amino acid residues in a plurality of primary variant positions from said primary sequences;

c) combining a plurality of said amino acid residues from said probability distribution to generate a secondary library of secondary sequences, wherein at least one of said secondary sequences is different from said primary sequences;

d) computationally ranking said secondary library and eliminating at least one unfavorable sequence from said secondary library ~~to generate a secondary library of secondary sequences comprising secondary variants~~ to generate a tertiary library; and

e) synthesizing a plurality of ~~said secondary~~ tertiary sequences to generate a ~~secondary~~ said tertiary library of scaffold protein variants.

5. (Original) A method according to claim 4 wherein said synthesizing is done by multiple PCR with pooled oligonucleotides.

6. (Original) A method according to 5 wherein said pooled oligonucleotides are added in equimolar amounts.

7. (Currently Amended) A method according to claim 5 wherein said pooled oligonucleotides are added in amounts that correspond to the frequency of the ~~mutation~~ amino acid residues from said probability distribution.

8. (Original) A method according to claim 6 wherein said pooled oligonucleotides are pooled in relative amounts.

9. (New) A method for generating a secondary library of scaffold protein variants comprising:

a) generating a library of primary sequences utilizing an alignment program;

b) generating a probability distribution of amino acid residues in a plurality of primary variant positions from said primary sequences;

c) combining a plurality of said amino acid residues from said probability distribution to generate a secondary library of secondary sequences, wherein at least one of said secondary sequences is different from said primary sequences; and

d) synthesizing a plurality of said secondary sequences to generate a secondary library of scaffold protein variants.